the resulting protein has a Leucine at position 2 instead of a Serine. This change at position 2 is reflected in SEQ ID NO:70.

II. Allowed claims

Applicants acknowledge that claim 107 is allowed and that claims 102-104 would be allowable if recited as independent claims. In this response, Claim 102 has been rewritten in independent format and claims 103 and 104 are made dependant therefrom.

III. Rejection under 35 U.S.C. § 112, first paragraph

Claims 100-104 are rejected as containing subject matter which was not described in the specification in such a way as to enable one skilled in the art to which it pertains, or with which it is most nearly connected, to make and/or use the invention. The Examiner indicated that claims 102-104 could be allowed if written as independent claims. Applicants respectfully traverse this rejection with respect to claims 100 and 101.

The antibody described in the Specification is directed towards the EPSPS enzyme from *Agrobacterium* sp. strain CP4 (SEQ ID NO:3). This enzyme was characterized by the inventors as belonging to a new sub-group of EPSPS enzymes named Class II EPSPS, as opposed to the Class I sub-group comprising EPSPS more similar to the *E. coli* enzyme. Although it is true that the similarity between the enzymes of the two classes is very low (Specification page 42, line 13), the similarity/identity of the enzymes within the same class is extremely high (Specification page 42, line 10). Therefore, an antibody directed against one member of the Class II enzyme is predicted to react against other members of that same group.

The obtaining and the screening of antibodies are well known by one skilled in the art and the standard techniques allow the screening of high number of antibodies in an efficient manner. This would not constitute undue experimentation.

Additionally, the seven catalytically important peptide domains described within the structure of EPSPS enzyme of Class II were identified by several methods including aligning the amino acid sequences of different Class I EPSPS with the crystal structure of Class I *E. coli* and Class II CP4 EPSPS, as well as locating those regions within the crystal structure of substrate-bound Class II EPSPS CP4 (Specification pages 47-50). Four of those regions (SEQ ID NOs:37-40) were actually deemed important in maintaining the substrate-binding and glyphosate-resistance capacities. Therefore, the domains claimed in claim 100 do actually correspond to naturally occurring sequences in polypeptides showing EPSPS activity (*see* Table IVB, Specification page 46).

Therefore, the rejection under 35 U.S.C. §112, first paragraph, should be withdrawn.

IV. Sequence Listing

Applicants respectfully request that the sequence listing currently in the file be replaced by the sequence listing hereby attached. A statement as requested under 37 C.F.R. § 1.825(a) and (b) and under 37 C.F.R. § 1.821(g) is also attached.

V. Conclusion

In view of the above Remarks, Applicant believes that all objections and rejections have been overcome and that the case is now in condition for allowance.

It is believed that no fee is due; however, should any fees under 37 C.F.R. §§ 1.16 to 1.21 be required for any reason relating to this document, the Commissioner is authorized to deduct said fees from our Deposit Account No. 01-2508/11899.0175.DVUS01.

The Examiner is invited to contact the undersigned attorney at (713) 787-1438 with any comments relating to this application.

Respectfully submitted,

Patricia A. Kammerer
Reg. No. 29,775
Attorney for Assignee
MONSANTO COMPANY

HOWREY SIMON ARNOLD & WHITE, LLP
750 Bering Drive
Houston, Texas 77057-2198
(713) 787-1400

Date: June 25, 2001

Marked-up version of the replaced paragraph in the Specification

--A CTP-CP4 EPSPS fusion was constructed between the *Arabidopsis thaliana* EPSPS CTP (Klee *et al.*, 1987) and the CP4 EPSPS coding sequences. The *Arabidopsis* CTP was engineered by site-directed mutagenesis to place a *Sph*I restriction site at the CTP processing site. This mutagenesis replaced the Glu-Lys at this location with Cyst-Met. The sequence of this CTP, designated as CTP2 (SEQ ID NO:10), is shown in Figure 9. The N-terminus of the CP4 EPSPS gene was modified to place a *Sph*I site that spans the Met codon. The second codon was converted to one for leucine in this step also. **This change is reflected in SEQ ID NO:70**. This change had no apparent effect on the in vivo activity of CP4 EPSPS in *E. coli* as judged by rate of complementation of the AroA allele. This modified N-terminus was then combined with the *Sac*I C-terminus and cloned downstream of the CTP2 sequences. The CTP2-CP4 EPSPS fusion was cloned into pBlueScript KS (+). This vector may be transcribed in vitro using the T7 polymerase and the RNA translated with ^{35}S-Methionine to provide material that may be evaluated for import into chloroplasts isolated from *Lactuca sativa* using the methods described hereinafter (della-Cioppa *et al.*, 1986, 1987). This template was transcribed in vitro using T7 polymerase and the ^{35}S-Methionine-labeled CTP2-CP4 EPSPS material was shown to import into chloroplasts with an efficiency comparable to that for the control Petunia EPSPS (control = ^{35}S labeled PreEPSPS [pMON6140: della-Cioppa *et al.*, 1986]).--

Marked-up version of the pending claims after amendments

102. An [~~The~~] antibody [~~of claim 100~~] **immunoreactive with a 5-enolpyruvylshikimate-3-phosphate synthase enzyme**, wherein the enzyme comprises SEQ ID NO:3 **or SEQ ID NO:70**.

103. The antibody of claim [~~100~~] **102**, further defined as a polyclonal antibody.

104. The antibody of claim [~~100~~] **102**, further defined as a monoclonal antibody.

107. A kit for the detection of a 5-enolpyruvylshikimate-3-phosphate synthase enzyme in a sample, said kit comprising:

a container comprising an antibody immunoreactive with SEQ ID NO:3 **or SEQ ID NO:70**; and

a detection agent.